



- 68 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gilula, Norton B
Cravatt, Benjamin F
Lerner, Richard A
- (ii) TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: The Scripps Research Institute
 - (B) STREET: 10550 North Torrey Pines Road
 - (C) CITY: La Jolla
 - (D) STATE: California
 - (E) COUNTRY: US
 - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/743,168
 - (B) FILING DATE: 04-NOV-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/489,535
 - (B) FILING DATE: 12-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fitting, Thomas
 - (B) REGISTRATION NUMBER: 34,163
 - (C) REFERENCE/DOCKET NUMBER: TSRI 485.2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 784-2937
 - (B) TELEFAX: (619) 784-9399

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 783 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGC CCA GGA GGT TCC TCA GGG GGT GAG GGG GCT CTC ATT GGA TCT GGA	48
Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly	
1 5 10 15	
GGT TCC CCT CTG GGT TTA GGC ACT GAC ATT GGC GGC AGC ATC CGG TTC	96
Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe	
20 25 30	
CCT TCT GCC TTC TGC GGC ATC TGT GGC CTC AAG CCT ACT GGC AAC CGC	144
Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr Gly Asn Arg	
35 40 45	
CTC AGC AAG AGT GGC CTG AAG GGC TGT GTC TAT GGA CAG ACG GCA GTG	192
Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val	
50 55 60	
CAG CTT TCT CTT GGC CCC ATG GCC CGG GAT GTG GAG AGC CTG GCG CTA	240
Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu Ser Leu Ala Leu	
65 70 75 80	
TGC CTG AAA GCT CTA CTG TGT GAG CAC TTG TTC ACC TTG GAC CCT ACC	288
Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr Leu Asp Pro Thr	
85 90 95	
GTG CCT CCC TTT CCC TTC AGA GAG GAG GTC TAT AGA AGT TCT AGA CCC	336
Val Pro Pro Phe Pro Phe Arg Glu Glu Val Tyr Arg Ser Ser Arg Pro	
100 105 110	
CTG CGT GTG GGG TAC TAT GAG ACT GAC AAC TAT ACC ATG CCC AGC CCA	384
Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr Met Pro Ser Pro	
115 120 125	
GCT ATG AGG AGG GCT CTG ATA GAG ACC AAG CAG AGA CTT GAG GCT GCT	432
Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg Leu Glu Ala Ala	

130	135	140	
GGC CAC ACG CTG ATT CCC TTC TTA CCC AAC AAC ATA CCC TAC GCC CTG			480
Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile Pro Tyr Ala Leu			
145	150	155	160
GAG GTC CTG TCT GCG GGC GGC CTG TTC AGT GAC GGT GGC CGC AGT TTT			528
Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly Gly Arg Ser Phe			
	165	170	175
CTC CAA AAC TTC AAA GGT GAC TTT GTG GAT CCC TGC TTG GGA GAC CTG			576
Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys Leu Gly Asp Leu			
	180	185	190
ATC TTA ATT CTG AGG CTG CCC AGC TGG TTT AAA AGA CTG CTG AGC CTC			624
Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg Leu Leu Ser Leu			
	195	200	205
CTG CTG AAG CCT CTG TTT CCT CGG CTG GCA GCC TTT CTC AAC AGT ATG			672
Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe Leu Asn Ser Met			
	210	215	220
CGT CCT CGG TCA GCT GAA AAG CTG TGG AAA CTG CAG CAT GAG ATT GAG			720
Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln His Glu Ile Glu			
	225	230	235
ATG TAT CGC CAG TCT GTG ATT GCC CAG TGG AAA GCG ATG AAC TTG GAT			768
Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn Leu Asp			
	245	250	255
GTG CTG CTG ACC TAA			783
Val Leu Leu Thr			
	260		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Glu	Gly	Ala	Leu	Ile	Gly	Ser	Gly
1				5				10						15	
Gly	Ser	Pro	Leu	Gly	Leu	Gly	Thr	Asp	Ile	Gly	Gly	Ser	Ile	Arg	Phe
			20					25						30	

Pro	Ser	Ala	Phe	Cys	Gly	Ile	Cys	Gly	Leu	Lys	Pro	Thr	Gly	Asn	Arg
		35					40					45			
Leu	Ser	Lys	Ser	Gly	Leu	Lys	Gly	Cys	Val	Tyr	Gly	Gln	Thr	Ala	Val
	50					55					60				
Gln	Leu	Ser	Leu	Gly	Pro	Met	Ala	Arg	Asp	Val	Glu	Ser	Leu	Ala	Leu
65					70					75					80
Cys	Leu	Lys	Ala	Leu	Leu	Cys	Glu	His	Leu	Phe	Thr	Leu	Asp	Pro	Thr
			85						90					95	
Val	Pro	Pro	Phe	Pro	Phe	Arg	Glu	Glu	Val	Tyr	Arg	Ser	Ser	Arg	Pro
			100						105					110	
Leu	Arg	Val	Gly	Tyr	Tyr	Glu	Thr	Asp	Asn	Tyr	Thr	Met	Pro	Ser	Pro
		115					120					125			
Ala	Met	Arg	Arg	Ala	Leu	Ile	Glu	Thr	Lys	Gln	Arg	Leu	Glu	Ala	Ala
	130					135					140				
Gly	His	Thr	Leu	Ile	Pro	Phe	Leu	Pro	Asn	Asn	Ile	Pro	Tyr	Ala	Leu
145					150					155					160
Glu	Val	Leu	Ser	Ala	Gly	Gly	Leu	Phe	Ser	Asp	Gly	Gly	Arg	Ser	Phe
				165					170					175	
Leu	Gln	Asn	Phe	Lys	Gly	Asp	Phe	Val	Asp	Pro	Cys	Leu	Gly	Asp	Leu
			180					185					190		
Ile	Leu	Ile	Leu	Arg	Leu	Pro	Ser	Trp	Phe	Lys	Arg	Leu	Leu	Ser	Leu
	195						200						205		
Leu	Leu	Lys	Pro	Leu	Phe	Pro	Arg	Leu	Ala	Ala	Phe	Leu	Asn	Ser	Met
	210					215					220				
Arg	Pro	Arg	Ser	Ala	Glu	Lys	Leu	Trp	Lys	Leu	Gln	His	Glu	Ile	Glu
225					230					235					240
Met	Tyr	Arg	Gln	Ser	Val	Ile	Ala	Gln	Trp	Lys	Ala	Met	Asn	Leu	Asp
				245					250					255	
Val	Leu	Leu	Thr												
			260												

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCGG NGGNGARGGN GC

22

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Gly Glu Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly Gly Ser
1 5 10 15

Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe Pro
20 25 30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Leu Ile Gly Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly	Leu	Gly	Thr	Asp	Ile	Gly	Gly	Ser	Ile	Arg	Phe	Pro	Ser	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg	Phe	Pro	Ser	Ala	Phe	Cys	Gly	Ile	Cys	Gly	Leu	Lys	Pro	Thr
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly	Leu	Lys	Pro	Thr	Gly	Asn	Arg	Leu	Ser	Lys	Ser	Gly	Leu	Lys
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys	Ser	Gly	Leu	Lys	Gly	Cys	Val	Tyr	Gly	Gln	Thr	Ala	Val	Gln
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gln	Thr	Ala	Val	Gln	Leu	Ser	Leu	Gly	Pro	Met	Ala	Arg	Asp	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	Arg	Asp	Val	Glu	Ser	Leu	Ala	Leu	Cys	Leu	Lys	Ala	Leu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys	Leu	Lys	Ala	Leu	Leu	Cys	Glu	His	Leu	Phe	Thr	Leu	Asp	Pro
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe	Thr	Leu	Asp	Pro	Thr	Val	Pro	Pro	Phe	Pro	Phe	Arg	Glu	Glu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro	Phe	Arg	Glu	Glu	Val	Tyr	Arg	Ser	Ser	Arg	Pro	Leu	Arg	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg	Pro	Leu	Arg	Val	Gly	Tyr	Tyr	Glu	Thr	Asp	Asn	Tyr	Thr	Met
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp	Asn	Tyr	Thr	Met	Pro	Ser	Pro	Ala	Met	Arg	Arg	Ala	Leu	Ile
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg	Arg	Ala	Leu	Ile	Glu	Thr	Lys	Gln	Arg	Leu	Glu	Ala	Ala	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu	Glu	Ala	Ala	Gly	His	Thr	Leu	Ile	Pro	Phe	Leu	Pro	Asn	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Phe	Leu	Pro	Asn	Asn	Ile	Pro	Tyr	Ala	Leu	Glu	Val	Leu	Ser	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu	Val	Leu	Ser	Ala	Gly	Gly	Leu	Phe	Ser	Asp	Gly	Gly	Arg	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asp	Gly	Gly	Arg	Ser	Phe	Leu	Gln	Asn	Phe	Lys	Gly	Asp	Phe	Val
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys	Gly	Asp	Phe	Val	Asp	Pro	Cys	Leu	Gly	Asp	Leu	Ile	Leu	Ile
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp	Leu	Ile	Leu	Ile	Leu	Arg	Leu	Pro	Ser	Trp	Phe	Lys	Arg	Leu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Trp	Phe	Lys	Arg	Leu	Leu	Ser	Leu	Leu	Lys	Pro	Leu	Phe	Pro
1				5				10				15	

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys	Pro	Leu	Phe	Pro	Arg	Leu	Ala	Ala	Phe	Leu	Asn	Ser	Met	Arg
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Asn Ser Met Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Lys Leu Trp Lys Leu Gln His Glu Ile Glu Met Tyr Arg Gln Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Lys	Ala	Met	Asn	Leu	Asp	Val	Leu	Leu	Thr	Pro	Met	Leu	Gly	Pro
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Pro	Met	Leu	Gly	Pro	Ala	Leu	Asp	Leu	Asn	Thr	Pro	Gly	Arg
1				5					10				

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGGATCCGG CATNGTRTAR TTRTC

25

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Asn Tyr Thr Met Pro
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 50..1789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTTTGTGCG AGCCGAGTTC TCTCGGGTGG CGGTCGGCTG CAGGAGATC ATG GTG	55
Met Val	
1	
CTG AGC GAA GTG TGG ACC ACG CTG TCT GGG GTC TCC GGG GTT TGC CTA	103
Leu Ser Glu Val Trp Thr Thr Leu Ser Gly Val Ser Gly Val Cys Leu	
5 10 15	
GCC TGC AGC TTG TTG TCG GCG GCG GTG GTC CTG CGA TGG ACC GGG CGC	151
Ala Cys Ser Leu Leu Ser Ala Ala Val Val Leu Arg Trp Thr Gly Arg	
20 25 30	
CAG AAG GCC CGG GGC GCG GCG ACC AGG GCG CGG CAG AAG CAG CGA GCC	199
Gln Lys Ala Arg Gly Ala Ala Thr Arg Ala Arg Gln Lys Gln Arg Ala	
35 40 45 50	
AGC CTG GAG ACC ATG GAC AAG GCG GTG CAG CGC TTC CGG CTG CAG AAT	247
Ser Leu Glu Thr Met Asp Lys Ala Val Gln Arg Phe Arg Leu Gln Asn	
55 60 65	

CCT GAC CTG GAC TCG GAG GCC TTG CTG ACC CTG CCC CTA CTC CAA CTG	295
Pro Asp Leu Asp Ser Glu Ala Leu Leu Thr Leu Pro Leu Leu Gln Leu	
70 75 80	
GTA CAG AAG TTA CAG AGT GGA GAG CTG TCC CCA GAG GCT GTG TTC TTT	343
Val Gln Lys Leu Gln Ser Gly Glu Leu Ser Pro Glu Ala Val Phe Phe	
85 90 95	
ACT TAC CTG GGA AAG GCC TGG GAA GTG AAC AAA GGG ACC AAC TGC GTG	391
Thr Tyr Leu Gly Lys Ala Trp Glu Val Asn Lys Gly Thr Asn Cys Val	
100 105 110	
ACC TCC TAT CTG ACC GAC TGT GAG ACT CAG CTG TCC CAG GCC CCA CGG	439
Thr Ser Tyr Leu Thr Asp Cys Glu Thr Gln Leu Ser Gln Ala Pro Arg	
115 120 125 130	
CAG GGC CTG CTC TAT GGT GTC CCT GTG AGC CTC AAG GAA TGC TTC AGC	487
Gln Gly Leu Leu Tyr Gly Val Pro Val Ser Leu Lys Glu Cys Phe Ser	
135 140 145	
TAC AAG GGC CAC GAC TCC ACA CTG GGC TTG AGC CTG AAT GAG GGC ATG	535
Tyr Lys Gly His Asp Ser Thr Leu Gly Leu Ser Leu Asn Glu Gly Met	
150 155 160	
CCA TCG GAA TCT GAC TGT GTG GTG GTG CAA GTG TTG AAG CTG CAG GGA	583
Pro Ser Glu Ser Asp Cys Val Val Val Gln Val Leu Lys Leu Gln Gly	
165 170 175	
GCT GTG CCC TTT GTG CAT ACC AAT GTC CCC CAG TCC ATG TTA AGC TTT	631
Ala Val Pro Phe Val His Thr Asn Val Pro Gln Ser Met Leu Ser Phe	
180 185 190	
GAC TGC AGT AAC CCT CTC TTT GGC CAG ACC ATG AAC CCA TGG AAG TCC	679
Asp Cys Ser Asn Pro Leu Phe Gly Gln Thr Met Asn Pro Trp Lys Ser	
195 200 205 210	
TCC AAG AGC CCA GGA GGT TCC TCA GGG GGT GAG GGG GCT CTC ATT GGA	727
Ser Lys Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly	
215 220 225	
TCT GGA GGT TCC CCT CTG GGT TTA GGC ACT GAC ATT GGC GGC AGC ATC	775
Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile	
230 235 240	
CGG TTC CCT TCT GCC TTC TGC GGC ATC TGT GGC CTC AAG CCT ACT GGC	823
Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr Gly	
245 250 255	
AAC CGC CTC AGC AAG AGT GGC CTG AAG GGC TGT GTC TAT GGA CAG ACG	871
Asn Arg Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr	
260 265 270	

GCA GTG CAG CTT TCT CTT GGC CCC ATG GCC CGG GAT GTG GAG AGC CTG Ala Val Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu Ser Leu 275 280 285 290	919
GCG CTA TGC CTG AAA GCT CTA CTG TGT GAG CAC TTG TTC ACC TTG GAC Ala Leu Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr Leu Asp 295 300 305	967
CCT ACC GTG CCT CCC TTG CCC TTC AGA GAG GAG GTC TAT AGA AGT TCT Pro Thr Val Pro Pro Leu Pro Phe Arg Glu Glu Val Tyr Arg Ser Ser 310 315 320	1015
AGA CCC CTG CGT GTG GGG TAC TAT GAG ACT GAC AAC TAT ACC ATG CCC Arg Pro Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr Met Pro 325 330 335	1063
AGC CCA GCT ATG AGG AGG GCT CTG ATA GAG ACC AAG CAG AGA CTT GAG Ser Pro Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg Leu Glu 340 345 350	1111
GCT GCT GGC CAC ACG CTG ATT CCC TTC TTA CCC AAC AAC ATA CCC TAC Ala Ala Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile Pro Tyr 355 360 365 370	1159
GCC CTG GAG GTC CTG TCT GCG GGC GGC CTG TTC AGT GAC GGT GGC CGC Ala Leu Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly Gly Arg 375 380 385	1207
AGT TTT CTC CAA AAC TTC AAA GGT GAC TTT GTG GAT CCC TGC TTG GGA Ser Phe Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys Leu Gly 390 395 400	1255
GAC CTG ATC TTA ATT CTG AGG CTG CCC AGC TGG TTT AAA AGA CTG CTG Asp Leu Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg Leu Leu 405 410 415	1303
AGC CTC CTG CTG AAG CCT CTG TTT CCT CGG CTG GCA GCC TTT CTC AAC Ser Leu Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe Leu Asn 420 425 430	1351
AGT ATG CGT CCT CGG TCA GCT GAA AAG CTG TGG AAA CTG CAG CAT GAG Ser Met Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln His Glu 435 440 445 450	1399
ATT GAG ATG TAT CGC CAG TCT GTG ATT GCC CAG TGG AAA GCG ATG AAC Ile Glu Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn 455 460 465	1447
TTG GAT GTG CTG CTG ACC CCC ATG TTG GGC CCT GCT CTG GAT TTG AAC Leu Asp Val Leu Leu Thr Pro Met Leu Gly Pro Ala Leu Asp Leu Asn 470 475 480	1495

ACA CCG GGC AGA GCC ACA GGG GCT ATC AGC TAC ACC GTT CTC TAC AAC Thr Pro Gly Arg Ala Thr Gly Ala Ile Ser Tyr Thr Val Leu Tyr Asn 485 490 495	1543
TGC CTG GAC TTC CCT GCG GGG GTG GTG CCT GTC ACC ACT GTG ACC GCC Cys Leu Asp Phe Pro Ala Gly Val Val Pro Val Thr Thr Val Thr Ala 500 505 510	1591
GAG GAC GAT GCC CAG ATG GAA CTC TAC AAA GGC TAC TTT GGG GAT ATC Glu Asp Asp Ala Gln Met Glu Leu Tyr Lys Gly Tyr Phe Gly Asp Ile 515 520 525 530	1639
TGG GAC ATC ATC CTG AAG AAG GCC ATG AAA AAT AGT GTC GGT CTG CCT Trp Asp Ile Ile Leu Lys Lys Ala Met Lys Asn Ser Val Gly Leu Pro 535 540 545	1687
GTG GCT GTG CAG TGC GTG GCT CTG CCC TGG CAG GAA GAG CTG TGT CTG Val Ala Val Gln Cys Val Ala Leu Pro Trp Gln Glu Glu Leu Cys Leu 550 555 560	1735
AGG TTC ATG CGG GAG GTG GAA CAG CTG ATG ACC CCT CAA AAG CAG CCA Arg Phe Met Arg Glu Val Glu Gln Leu Met Thr Pro Gln Lys Gln Pro 565 570 575	1783
TCG TGAGGGTCGT TCATCCGCCA GCTCTGGAGG ACCTAAGGCC CATGCGCTGT Ser 580	1836
GCACTGTAGC CCCATGTATT CAGGAGCCAC CACCCACGAG GGAACGCCCA GCACAGGGAA	1896
GAGGTGTCTA CCTGCCCTCC CCTGGACTCC TGCAGCCACA ACCAAGTCTG GACCTTCCTC	1956
CCCGTTATGG TCTACTTTCC ATCCTGATTC CCTGCTTTTT ATGGCAGCCA GCAGGAATGA	2016
CGTGGGCCAA GGATCACCAA CATTCAAAAA CAATGCGTTT ATCTATTTTC TGGGTATCTC	2076
CATTAGGGCC CTGGGAACCA GAGTGCTGGG AAGGCTGTCC AGACCCTCCA GAGCTGGCTG	2136
TAACCACATC ACTCTCCTGC TCCAAAGCCT CCCTAGTTCT GTCACCCACA AGATAGACAC	2196
AGGGACATGT CCTTGGCACT TGA CTCTGT CTTCTCTTTC TTATTCAGAT TGACCCAGC	2256
CTTGATGGAC CCTGCCCCTG CACTTCCTTC CTCAGTCCAC CTCTCTGCCG ACACGCCCTT	2316
TTTATGGCTC CTCTATTTGT TGTGGAGACA AGGTTTCTCT CAGTAGCCCT GGCTGTCCAG	2376
GACCTCACTC TGTAGATGAG GCTGGCTTTC AACTCACAAG GCTGCCTGCC TGGGTGCTGG	2436
GATTAAAGGC GTATGCCACC ACAAAGAAAA AAAAAA	2472

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Val	Leu	Ser	Glu	Val	Trp	Thr	Thr	Leu	Ser	Gly	Val	Ser	Gly	Val	
1				5					10					15		
Cys	Leu	Ala	Cys	Ser	Leu	Leu	Ser	Ala	Ala	Val	Val	Leu	Arg	Trp	Thr	
			20					25					30			
Gly	Arg	Gln	Lys	Ala	Arg	Gly	Ala	Ala	Thr	Arg	Ala	Arg	Gln	Lys	Gln	
		35					40					45				
Arg	Ala	Ser	Leu	Glu	Thr	Met	Asp	Lys	Ala	Val	Gln	Arg	Phe	Arg	Leu	
		50				55					60					
Gln	Asn	Pro	Asp	Leu	Asp	Ser	Glu	Ala	Leu	Leu	Thr	Leu	Pro	Leu	Leu	
65					70					75					80	
Gln	Leu	Val	Gln	Lys	Leu	Gln	Ser	Gly	Glu	Leu	Ser	Pro	Glu	Ala	Val	
				85					90					95		
Phe	Phe	Thr	Tyr	Leu	Gly	Lys	Ala	Trp	Glu	Val	Asn	Lys	Gly	Thr	Asn	
		100						105					110			
Cys	Val	Thr	Ser	Tyr	Leu	Thr	Asp	Cys	Glu	Thr	Gln	Leu	Ser	Gln	Ala	
		115					120					125				
Pro	Arg	Gln	Gly	Leu	Leu	Tyr	Gly	Val	Pro	Val	Ser	Leu	Lys	Glu	Cys	
		130				135					140					
Phe	Ser	Tyr	Lys	Gly	His	Asp	Ser	Thr	Leu	Gly	Leu	Ser	Leu	Asn	Glu	
145					150					155					160	
Gly	Met	Pro	Ser	Glu	Ser	Asp	Cys	Val	Val	Val	Gln	Val	Leu	Lys	Leu	
				165					170					175		
Gln	Gly	Ala	Val	Pro	Phe	Val	His	Thr	Asn	Val	Pro	Gln	Ser	Met	Leu	
		180						185					190			
Ser	Phe	Asp	Cys	Ser	Asn	Pro	Leu	Phe	Gly	Gln	Thr	Met	Asn	Pro	Trp	
		195					200					205				
Lys	Ser	Ser	Lys	Ser	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Glu	Gly	Ala	Leu	

210	215	220
Ile Gly Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly		
225	230	235 240
Ser Ile Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro		
	245	250 255
Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly		
	260	265 270
Gln Thr Ala Val Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu		
	275	280 285
Ser Leu Ala Leu Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr		
	290	295 300
Leu Asp Pro Thr Val Pro Pro Leu Pro Phe Arg Glu Glu Val Tyr Arg		
305	310	315 320
Ser Ser Arg Pro Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr		
	325	330 335
Met Pro Ser Pro Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg		
	340	345 350
Leu Glu Ala Ala Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile		
	355	360 365
Pro Tyr Ala Leu Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly		
	370	375 380
Gly Arg Ser Phe Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys		
385	390	395 400
Leu Gly Asp Leu Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg		
	405	410 415
Leu Leu Ser Leu Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe		
	420	425 430
Leu Asn Ser Met Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln		
	435	440 445
His Glu Ile Glu Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala		
	450	455 460
Met Asn Leu Asp Val Leu Leu Thr Pro Met Leu Gly Pro Ala Leu Asp		
465	470	475 480
Leu Asn Thr Pro Gly Arg Ala Thr Gly Ala Ile Ser Tyr Thr Val Leu		

485 490 495

Tyr Asn Cys Leu Asp Phe Pro Ala Gly Val Val Pro Val Thr Thr Val
500 505 510

Thr Ala Glu Asp Asp Ala Gln Met Glu Leu Tyr Lys Gly Tyr Phe Gly
515 520 525

Asp Ile Trp Asp Ile Ile Leu Lys Lys Ala Met Lys Asn Ser Val Gly
530 535 540

Leu Pro Val Ala Val Gln Cys Val Ala Leu Pro Trp Gln Glu Glu Leu
545 550 555 560

Cys Leu Arg Phe Met Arg Glu Val Glu Gln Leu Met Thr Pro Gln Lys
565 570 575

Gln Pro Ser

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTTTTTTTT CTTTGTGGTG GCATACGCCT TTAATCCCAG CACCCAGGCA GGCAGCCTTG	60
TGAGTTGAAA GCCAGCCTCA TCTACAGAGT GAGGTCCTGG ACAGCCAGGG CTACTGAGAG	120
AAACCTTGTC TCCACAACAA ATAGAGGAGC CATAAAAAGG GCGTGTCGGC AGAGAGGTGG	180
ACTGAGGAAG GAAGTGCAGG GGCAGGGTCC ATCAAGGCTG GGGTCAATCT GAATAAGAAA	240
GGAAGGACAG GAGTCAAGTG CCAAGGACAT GTCCCTGTGT CTATCTTGTG GGTGACAGAA	300
CTAGGGAGGC TTTGGAGCAG GAGAGTGATG TGTTACAGC CAGCTCTGGA GGGTCTGGAC	360

AGCCTTCCCA	GCACTCTGGT	TCCCAGGGCC	CTAATGGAGA	TACCCAGAAA	ATAGATAAAC	420
GCATTGTTTT	TGAATGTTGG	TGATCCTTGG	CCCACGTCAT	TCCTGCTGGC	TGCCATAAAA	480
AGCAGGGAAT	CAGGATGGAA	AGTAGACCAT	AACGGGGAGG	AAGGTCCAGA	CTTGTTGTG	540
GCTGCAGGAG	TCCAGGGGAG	GGCAGGTAGA	CACCTCTTCC	CTGTGCTGGG	CGTTCCCTCG	600
TGGGTGGTGG	CTCCTGAATA	CATGGGGCTA	CAGTGCACAG	CGCATGGGCC	TTAGGTCCTC	660
CAGAGCTGGC	GGATGAACGA	CCCTCACGAT	GGCTGCTTTT	GAGGGGTCAT	CAGCTGTTCC	720
ACCTCCCSCA	TGAACCTCAG	ACACAGCTCT	TCCTGCCAGG	GCAGAGCCAC	GCACTGCACA	780
GCCACAGGCA	GACCGACACT	ATTTTTCATG	GCCTTCTTCA	GGATGATGTC	CCAGATATCC	840
CCAAAGTAGC	CTTTGTAGAG	TTCCATCTGG	GCATCGTCCT	CGGCGGTCAC	AGTGGTGACA	900
GGCACCACCC	CCGCAGGGAA	GTCCAGGCAG	TTGTAGAGAA	CGGTGTAGCT	GATAGCCCCT	960
GTGGCTCTGC	CCGGTGTGTT	CAAATCCAGA	GCAGGGCCCA	ACATGGGGGT	CAGCAGCACA	1020
TCCAAGTTCA	TCGCTTTCCA	CTGGGCAATC	ACAGACTGGC	GATACATCTC	AATCTCATGC	1080
TGCAGTTTCC	ACAGCTTTTC	AGCTGACCGA	GGACGCATAC	TGTTGAGAAA	GGCTGCCAGC	1140
CGAGGAAACA	GAGGCTTCAG	CAGGAGGCTC	AGCAGTCTTT	TAAACCAGCT	GGGCAGCCTC	1200
AGAATTAAGA	TCAGGTCTCC	CAAGCAGGGA	TCCACAAAGT	CACCTTTGAA	GTTTTGGAGA	1260
AAACTGCGGC	CACCGTCACT	GAACAGGCCG	CCCGCAGACA	GGACCTCCAG	GGCGTAGGGT	1320
ATGTTGTTGG	GTAAGAAGGG	AATCAGCGTG	TGGCCAGCAG	CCTCAAGTCT	CTGCTTGGTC	1380
TCTATCAGAG	CCCTCCTCAT	AGCTGGGCTG	GGCATGGTAT	AGTTGTCAGT	CTCATAGTAC	1440
CCCACACGCA	GGGGTCTAGA	ACTTCTATAG	ACCTCCTCTC	TGAAGGGCAA	GGGAGGCACG	1500
GTAGGGTCCA	AGGTGAACAA	GTGCTCACAC	AGTAGAGCTT	TCAGGCATAG	CGCCAGGCTC	1560
TCCACATCCC	GGGCCATGGG	GCCAAGAGAA	AGCTGCACTG	CCGTCTGTCC	ATAGACACAG	1620
CCCTTCAGGC	CACTCTTGCT	GAGGCGGTTG	CCAGTAGGCT	TGAGGCCACA	GATGCCGCAG	1680
AAGGCAGAAG	GGAACCGGAT	GCTGCCGCCA	ATGTCAGTGC	CTAAACCCAG	AGGGGAACCT	1740
CCAGATCCAA	TGAGAGCCCC	CTCACCCCCT	GAGGAACCTC	CTGGGCTCTT	GGAGGACTTC	1800
CATGGGTTCA	TGGTCTGGCC	AAAGAGAGGG	TTACTGCAGT	CAAAGCTTAA	CATGGACTGG	1860
GGGACATTGG	TATGCACAAA	GGGCACAGCT	CCCTGCAGCT	TCAACACTTG	CACCACCACA	1920

CAGTCAGATT CCGATGGCAT GCCCTCATTC AGGCTCAAGC CCAGTGTGGA GTCGTGGCCC	1980
TTGTAGCTGA AGCATTCCTT GAGGCTCACA GGGACACCAT AGAGCAGGCC CTGCCGTGGG	2040
GCCTGGGACA GCTGAGTCTC ACAGTCGGTC AGATAGGAGG TCACGCAGTT GGTCCCTTTG	2100
TTCACTTCCC AGGCCTTTCC CAGGTAAGTA AAGAACACAG CCTCTGGGGA CAGCTCTCCA	2160
CTCTGTAACT TCTGTACCAG TTGGAGTAGG GGCAGGGTCA GCAAGGCCTC CGAGTCCAGG	2220
TCAGGATTCT GCAGCCGGAA GCGCTGCACC GCCTTGTCCA TGGTCTCCAG GCTGGCTCGC	2280
TGCTTCTGCC GCGCCCTGGT CGCCGCGCCC CGGGCCTTCT GGCGCCCGGT CCATCGCAGG	2340
ACCACCGCCG CCGACAACAA GCTGCAGGCT AGGCAAACCC CGGAGACCCC AGACAGCGTG	2400
GTCCACACTT CGCTCAGCAC CATGATCTCC TGCAGCCGAC CGCCACCCGA GAGAACTCGG	2460
CTCGCACAAA CC	2472

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Pro	Pro	Leu	Pro	Xaa	Arg
1				5	

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TGG	GTC	ATG	GTG	CTG	AGC	GAA	GTG	TGG	ACC	GCG	CTG	TCT	GGA	CTC	TCC	48
Trp	Val	Met	Val	Leu	Ser	Glu	Val	Trp	Thr	Ala	Leu	Ser	Gly	Leu	Ser	
1				5				10					15			
GGG	GTT	TGC	CTA	GCC	TGC	AGC	TTG	CTG	TCG	GCG	GCG	GTG	GTC	CTG	CGA	96
Gly	Val	Cys	Leu	Ala	Cys	Ser	Leu	Leu	Ser	Ala	Ala	Val	Val	Leu	Arg	
			20					25					30			
TGG	ACC	AGG	AGC	CAG	ACC	GCC	CGG	GGC	GCG	GTG	ACC	AGG	GCG	CGG	CAG	144
Trp	Thr	Arg	Ser	Gln	Thr	Ala	Arg	Gly	Ala	Val	Thr	Arg	Ala	Arg	Gln	
		35					40					45				
AAG	CAG	CGA	GCC	GGC	CTG	GAG	ACC	ATG	GAC	AAG	GCG	GTG	CAG	CGC	TTC	192
Lys	Gln	Arg	Ala	Gly	Leu	Glu	Thr	Met	Asp	Lys	Ala	Val	Gln	Arg	Phe	
	50					55					60					
CGG	CTG	CAG	AAT	CCT	GAC	CTG	GAT	TCA	GAG	GCC	TTG	CTG	GCT	CTG	CCC	240
Arg	Leu	Gln	Asn	Pro	Asp	Leu	Asp	Ser	Glu	Ala	Leu	Leu	Ala	Leu	Pro	
65					70					75					80	
CTG	CTC	CAA	CTG	GTA	CAG	AAG	TTA	CAG	AGT	GGG	GAA	CTG	TCC	CCA	GAA	288
Leu	Leu	Gln	Leu	Val	Gln	Lys	Leu	Gln	Ser	Gly	Glu	Leu	Ser	Pro	Glu	
			85					90					95			
GCT	GTG	CTC	TTT	ACC	TAC	CTG	GGA	AAG	GCC	TGG	GAA	GTG	AAC	AAA	GGG	336
Ala	Val	Leu	Phe	Thr	Tyr	Leu	Gly	Lys	Ala	Trp	Glu	Val	Asn	Lys	Gly	
		100						105					110			
ACC	AAC	TGT	GTG	ACC	TCC	TAT	CTG	ACT	GAC	TGT	GAG	ACT	CAG	CTG	TCC	384
Thr	Asn	Cys	Val	Thr	Ser	Tyr	Leu	Thr	Asp	Cys	Glu	Thr	Gln	Leu	Ser	
		115					120					125				
CAG	GCC	CCA	CGG	CAG	GGC	CTG	CTC	TAT	GGC	GTC	CCC	GTG	AGC	CTC	AAG	432
Gln	Ala	Pro	Arg	Gln	Gly	Leu	Leu	Tyr	Gly	Val	Pro	Val	Ser	Leu	Lys	
	130					135					140					
GAA	TGC	TTC	AGC	TAC	AAG	GGC	CAT	GCT	TCC	ACA	CTG	GGC	TTA	AGT	TTG	480
Glu	Cys	Phe	Ser	Tyr	Lys	Gly	His	Ala	Ser	Thr	Leu	Gly	Leu	Ser	Leu	
145					150				155					160		
AAC	GAG	GGT	GTG	ACA	TCG	GAG	AGT	GAC	TGT	GTG	GTG	GTG	CAG	GTA	CTG	528
Asn	Glu	Gly	Val	Thr	Ser	Glu	Ser	Asp	Cys	Val	Val	Val	Gln	Val	Leu	
			165					170					175			

AAG CTG CAG GGA GCT GTG CCC TTT GTG CAC ACC AAC GTC CCC CAG TCC	576
Lys Leu Gln Gly Ala Val Pro Phe Val His Thr Asn Val Pro Gln Ser	
180 185 190	
ATG CTA AGC TAT GAC TGC AGT AAC CCC CTC TTT GGC CAG ACC ATG AAC	624
Met Leu Ser Tyr Asp Cys Ser Asn Pro Leu Phe Gly Gln Thr Met Asn	
195 200 205	
CCG TGG AAG CCC TCC AAG AGT CCA GGA GGT TCC TCA GGG GGT GAG GGG	672
Pro Trp Lys Pro Ser Lys Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly	
210 215 220	
GCT CTC ATT GGA TCT GGA GGC TCC CCT CTG GGT TTA GGC ACT GAC ATC	720
Ala Leu Ile Gly Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile	
225 230 235 240	
GGC GGC AGC ATC CGG TTC CCT TCT GCC TTC TGT GGC ATC TGT GGC CTC	768
Gly Gly Ser Ile Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu	
245 250 255	
AAG CCT ACT GGG AAC CGC CTC AGC AAG AGT GGC CTG AAG AGC TGT GTT	816
Lys Pro Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys Ser Cys Val	
260 265 270	
TAT GGA CAG ACA GCA GTG CAG CTT TCT GTT GGC CCC ATG GCA CGG GAT	864
Tyr Gly Gln Thr Ala Val Gln Leu Ser Val Gly Pro Met Ala Arg Asp	
275 280 285	
GTG GAT AGC CTG GCA TTG TGC ATG AAA GCC CTA CTT TGT GAG GAT TTG	912
Val Asp Ser Leu Ala Leu Cys Met Lys Ala Leu Leu Cys Glu Asp Leu	
290 295 300	
TTC CGC TTG GAC TCC ACC ATC CCC CCC TTG CCC TTC AGG GAG GAG ATC	960
Phe Arg Leu Asp Ser Thr Ile Pro Pro Leu Pro Phe Arg Glu Glu Ile	
305 310 315 320	
TAC AGA AGT TCT CGA CCC CTT CGT GTG GGA TAC TAT GAA ACT GAC AAC	1008
Tyr Arg Ser Ser Arg Pro Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn	
325 330 335	
TAC ACC ATG CCC ACT CCA GCC ATG AGG AGG GCT GTG ATG GAG ACC AAG	1056
Tyr Thr Met Pro Thr Pro Ala Met Arg Arg Ala Val Met Glu Thr Lys	
340 345 350	
CAG AGT CTC GAG GCT GCT GGC CAC ACG CTG GTC CCC TTC TTA CCA AAC	1104
Gln Ser Leu Glu Ala Ala Gly His Thr Leu Val Pro Phe Leu Pro Asn	
355 360 365	
AAC ATA CCT TAT GCC CTG GAG GTC CTG TCG GCA GGT GGG CTG TTC AGT	1152
Asn Ile Pro Tyr Ala Leu Glu Val Leu Ser Ala Gly Gly Leu Phe Ser	
370 375 380	

GAT GGT GGC TGC TCT TTT CTC CAA AAC TTC AAA GGC GAC TTT GTG GAT Asp Gly Gly Cys Ser Phe Leu Gln Asn Phe Lys Gly Asp Phe Val Asp 385 390 395 400	1200
CCC TGC TTG GGG GAC CTG GTC TTA GTG CTG AAG CTG CCC AGG TGG TTT Pro Cys Leu Gly Asp Leu Val Leu Val Leu Lys Leu Pro Arg Trp Phe 405 410 415	1248
AAA AAA CTG CTG AGC TTC CTG CTG AAG CCT CTG TTT CCT CGG CTG GCA Lys Lys Leu Leu Ser Phe Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala 420 425 430	1296
GCC TTT CTC AAC AGT ATG TGT CCT CGG TCA GCC GAA AAG CTG TGG GAA Ala Phe Leu Asn Ser Met Cys Pro Arg Ser Ala Glu Lys Leu Trp Glu 435 440 445	1344
CTG CAG CAT GAG ATT GAG ATG TAT CGC CAG TCC GTC ATT GCC CAG TGG Leu Gln His Glu Ile Glu Met Tyr Arg Gln Ser Val Ile Ala Gln Trp 450 455 460	1392
AAG GCA ATG AAC TTG GAC GTG GTG CTA ACC CCC ATG CTG GGT CCT GCT Lys Ala Met Asn Leu Asp Val Val Leu Thr Pro Met Leu Gly Pro Ala 465 470 475 480	1440
CTG GAT TTG AAC ACA CCG GGC AGA GCC ACA GGG GCT ATC AGC TAC ACT Leu Asp Leu Asn Thr Pro Gly Arg Ala Thr Gly Ala Ile Ser Tyr Thr 485 490 495	1488
GTT CTC TAT AAC TGC CTG GAC TTC CCT GCG GGG GTG GTG CCT GTC ACC Val Leu Tyr Asn Cys Leu Asp Phe Pro Ala Gly Val Val Pro Val Thr 500 505 510	1536
ACT GTG ACC GCT GAG GAC GAT GCC CAG ATG GAA CAC TAC AAA GGC TAC Thr Val Thr Ala Glu Asp Asp Ala Gln Met Glu His Tyr Lys Gly Tyr 515 520 525	1584
TTT GGG GAT ATG TGG GAC AAC ATT CTG AAG AAG GGC ATG AAA AAG GGT Phe Gly Asp Met Trp Asp Asn Ile Leu Lys Lys Gly Met Lys Lys Gly 530 535 540	1632
ATA GGC CTG CCT GTG GCT GTG CAG TGC GTG GCT CTG CCC TGG CAG GAA Ile Gly Leu Pro Val Ala Val Gln Cys Val Ala Leu Pro Trp Gln Glu 545 550 555 560	1680
GAG CTG TGT CTG CGG TTC ATG CGG GAG GTG GAA CGG CTG ATG ACC CCT Glu Leu Cys Leu Arg Phe Met Arg Glu Val Glu Arg Leu Met Thr Pro 565 570 575	1728
GAA AAG CGG CCA TCT TGAGGGTCAT TCATCTGCCC AGCTCTGGAG GACCTAAGGC Glu Lys Arg Pro Ser 580	1783

CCATGCGCTC TGCAGTGCAG CCCCATCTAT TCAGGATCCT GCCACCCATG AGGAGATGCC	1843
CAGCACGGGA AGAGGCAACC ACCTGCCCTC CCCTGGACTC CTACAGAAAC CCAGGACATG	1903
CCCTCCATAA CCAAGTCTGG ACCAGCTCCC CCGGAATTCC TGCAGCCCGG GGGATC	1959

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Trp	Val	Met	Val	Leu	Ser	Glu	Val	Trp	Thr	Ala	Leu	Ser	Gly	Leu	Ser	1	5	10	15
Gly	Val	Cys	Leu	Ala	Cys	Ser	Leu	Leu	Ser	Ala	Ala	Val	Val	Leu	Arg	20	25	30	
Trp	Thr	Arg	Ser	Gln	Thr	Ala	Arg	Gly	Ala	Val	Thr	Arg	Ala	Arg	Gln	35	40	45	
Lys	Gln	Arg	Ala	Gly	Leu	Glu	Thr	Met	Asp	Lys	Ala	Val	Gln	Arg	Phe	50	55	60	
Arg	Leu	Gln	Asn	Pro	Asp	Leu	Asp	Ser	Glu	Ala	Leu	Leu	Ala	Leu	Pro	65	70	75	80
Leu	Leu	Gln	Leu	Val	Gln	Lys	Leu	Gln	Ser	Gly	Glu	Leu	Ser	Pro	Glu	85	90	95	
Ala	Val	Leu	Phe	Thr	Tyr	Leu	Gly	Lys	Ala	Trp	Glu	Val	Asn	Lys	Gly	100	105	110	
Thr	Asn	Cys	Val	Thr	Ser	Tyr	Leu	Thr	Asp	Cys	Glu	Thr	Gln	Leu	Ser	115	120	125	
Gln	Ala	Pro	Arg	Gln	Gly	Leu	Leu	Tyr	Gly	Val	Pro	Val	Ser	Leu	Lys	130	135	140	
Glu	Cys	Phe	Ser	Tyr	Lys	Gly	His	Ala	Ser	Thr	Leu	Gly	Leu	Ser	Leu	145	150	155	160
Asn	Glu	Gly	Val	Thr	Ser	Glu	Ser	Asp	Cys	Val	Val	Val	Gln	Val	Leu	165	170	175	

Lys Leu Gln Gly Ala Val Pro Phe Val His Thr Asn Val Pro Gln Ser
180 185 190

Met Leu Ser Tyr Asp Cys Ser Asn Pro Leu Phe Gly Gln Thr Met Asn
195 200 205

Pro Trp Lys Pro Ser Lys Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly
210 215 220

Ala Leu Ile Gly Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile
225 230 235 240

Gly Gly Ser Ile Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu
245 250 255

Lys Pro Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys Ser Cys Val
260 265 270

Tyr Gly Gln Thr Ala Val Gln Leu Ser Val Gly Pro Met Ala Arg Asp
275 280 285

Val Asp Ser Leu Ala Leu Cys Met Lys Ala Leu Leu Cys Glu Asp Leu
290 295 300

Phe Arg Leu Asp Ser Thr Ile Pro Pro Leu Pro Phe Arg Glu Glu Ile
305 310 315 320

Tyr Arg Ser Ser Arg Pro Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn
325 330 335

Tyr Thr Met Pro Thr Pro Ala Met Arg Arg Ala Val Met Glu Thr Lys
340 345 350

Gln Ser Leu Glu Ala Ala Gly His Thr Leu Val Pro Phe Leu Pro Asn
355 360 365

Asn Ile Pro Tyr Ala Leu Glu Val Leu Ser Ala Gly Gly Leu Phe Ser
370 375 380

Asp Gly Gly Cys Ser Phe Leu Gln Asn Phe Lys Gly Asp Phe Val Asp
385 390 395 400

Pro Cys Leu Gly Asp Leu Val Leu Val Leu Lys Leu Pro Arg Trp Phe
405 410 415

Lys Lys Leu Leu Ser Phe Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala
420 425 430

Ala Phe Leu Asn Ser Met Cys Pro Arg Ser Ala Glu Lys Leu Trp Glu
435 440 445

Leu Gln His Glu Ile Glu Met Tyr Arg Gln Ser Val Ile Ala Gln Trp
450 455 460

Lys Ala Met Asn Leu Asp Val Val Leu Thr Pro Met Leu Gly Pro Ala
465 470 475 480

Leu Asp Leu Asn Thr Pro Gly Arg Ala Thr Gly Ala Ile Ser Tyr Thr
485 490 495

Val Leu Tyr Asn Cys Leu Asp Phe Pro Ala Gly Val Val Pro Val Thr
500 505 510

Thr Val Thr Ala Glu Asp Asp Ala Gln Met Glu His Tyr Lys Gly Tyr
515 520 525

Phe Gly Asp Met Trp Asp Asn Ile Leu Lys Lys Gly Met Lys Lys Gly
530 535 540

Ile Gly Leu Pro Val Ala Val Gln Cys Val Ala Leu Pro Trp Gln Glu
545 550 555 560

Glu Leu Cys Leu Arg Phe Met Arg Glu Val Glu Arg Leu Met Thr Pro
565 570 575

Glu Lys Arg Pro Ser
580

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCCCCGG GCTGCAGGAA TTCCGGGGGA GCTGGTCCAG ACTTGGTTAT GGAGGGCATG	60
TCCTGGGTTT CTGTAGGAGT CCAGGGGAGG GCAGGTGGTT GCCTCTTCCC GTGCTGGGCA	120
TCTCCTCATG GGTGGCAGGA TCCTGAATAG ATGGGGCTGC AGTGCAGAGC GCATGGGCCT	180

TAGGTCCTCC	AGAGCTGGGC	AGATGAATGA	CCCTCAAGAT	GGCCGCTTTT	CAGGGGTCAT	240
CAGCCGTTCC	ACCTCCCGCA	TGAACCGCAG	ACACAGCTCT	TCCTGCCAGG	GCAGAGCCAC	300
GCACTGCACA	GCCACAGGCA	GGCCTATACC	CTTTTTCATG	CCCTTCTTCA	GAATGTTGTC	360
CCACATATCC	CCAAAGTAGC	CTTTGTAGTG	TTCCATCTGG	GCATCGTCCT	CAGCGGTCAC	420
AGTGGTGACA	GGCACCACCC	CCGCAGGGAA	GTCCAGGCAG	TTATAGAGAA	CAGTGTAGCT	480
GATAGCCCCCT	GTGGCTCTGC	CCGGTGTGTT	CAAATCCAGA	GCAGGACCCA	GCATGGGGGT	540
TAGCACCACG	TCCAAGTTCA	TTGCCTTCCA	CTGGGCAATG	ACGGACTGGC	GATACATCTC	600
AATCTCATGC	TGCAGTTCCC	ACAGCTTTTC	GGCTGACCGA	GGACACATAC	TGTTGAGAAA	660
GGCTGCCAGC	CGAGGAAACA	GAGGCTTCAG	CAGGAAGCTC	AGCAGTTTTT	TAAACCACCT	720
GGGCAGCTTC	AGCACTAAGA	CCAGGTCCCC	CAAGCAGGGA	TCCACAAAGT	CGCCTTTGAA	780
GTTTTGGAGA	AAAGAGCAGC	CACCATCACT	GAACAGCCCA	CCTGCCGACA	GGACCTCCAG	840
GGCATAAGGT	ATGTTGTTTG	GTAAGAAGGG	GACCAGCGTG	TGGCCAGCAG	CCTCGAGACT	900
CTGCTTGGTC	TCCATCACAG	CCCTCCTCAT	GGCTGGAGTG	GGCATGGTGT	AGTTGTCAGT	960
TTCATAGTAT	CCCACACGAA	GGGGTCGAGA	ACTTCTGTAG	ATCTCCTCCC	TGAAGGGCAA	1020
GGGGGGGATG	GTGGAGTCCA	AGCGGAACAA	ATCCTCACAA	AGTAGGGCTT	TCATGCACAA	1080
TGCCAGGCTA	TCCACATCCC	GTGCCATGGG	GCCAACAGAA	AGCTGCAC TG	CTGTCTGTCC	1140
ATAAACACAG	CTCTTCAGGC	CAC TCTTGCT	GAGGCGGTTC	CCAGTAGGCT	TGAGGCCACA	1200
GATGCCACAG	AAGGCAGAAG	GGAACCGGAT	GCTGCCGCCG	ATGTCAGTGC	CTAAACCCAG	1260
AGGGGAGCCT	CCAGATCCAA	TGAGAGCCCC	CTCACCCCCCT	GAGGAACCTC	CTGGACTCTT	1320
GGAGGGCTTC	CACGGGTTCA	TGGTCTGGCC	AAAGAGGGGG	TTACTGCAGT	CATAGCTTAG	1380
CATGGACTGG	GGGACGTTGG	TGTGCACAAA	GGGCACAGCT	CCCTGCAGCT	TCAGTACCTG	1440
CACCACCACA	CAGTCACTCT	CCGATGTCAC	ACCCTCGTTC	AAACTTAAGC	CCAGTG TGGA	1500
AGCATGGCCC	TTGTAGCTGA	AGCATTCCTT	GAGGCTCACG	GGGACGCCAT	AGAGCAGGCC	1560
CTGCCGTGGG	GCCTGGGACA	GCTGAGTCTC	ACAGTCAGTC	AGATAGGAGG	TCACACAGTT	1620
GGTCCCTTTG	TTCACTTCCC	AGGCC'TTTCC	CAGGTAGGTA	AAGAGCACAG	CTTCTGGGGA	1680
CAGTTCCCCA	CTCTGTAACT	TCTGTACCAG	TTGGAGCAGG	GGCAGAGCCA	GCAAGGCCTC	1740

TGAATCCAGG TCAGGATTCT GCAGCCGGAA GCGCTGCACC GCCTTGTCCA TGGTCTCCAG	1800
GCCGGCTCGC TGCTTCTGCC GCGCCCTGGT CACCGCGCCC CGGGCGGTCT GGCTCCTGGT	1860
CCATCGCAGG ACCACCGCCG CCGACAGCAA GCTGCAGGCT AGGCAAACCC CGGAGAGTCC	1920
AGACAGCGCG GTCCACACTT CGCTCAGCAC CATGACCCA	1959

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2045 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..1775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TG CCG GGC GGT AGG CAG CAG CAG GCT GAA GGG ATC ATG GTG CAG TAC	47
Pro Gly Gly Arg Gln Gln Gln Ala Glu Gly Ile Met Val Gln Tyr	
1 5 10 15	
GAG CTG TGG GCC GCG CTG CCT GGC GCC TCC GGG GTC GCC CTG GCC TGC	95
Glu Leu Trp Ala Ala Leu Pro Gly Ala Ser Gly Val Ala Leu Ala Cys	
20 25 30	
TGC TTC GTG GCG GCG GCC GTG GCC CTG CGC TGG TCC GGG CGC CGG ACG	143
Cys Phe Val Ala Ala Ala Val Ala Leu Arg Trp Ser Gly Arg Arg Thr	
35 40 45	
GCG CGG GGC GCG GTG GTC CGG GCG CGA CAG AAG CAG CGA GCG GGC CTG	191
Ala Arg Gly Ala Val Val Arg Ala Arg Gln Lys Gln Arg Ala Gly Leu	
50 55 60	
GAG AAC ATG GAC AGG GCG GCG CAG CGC TTC CGG CTC CAG AAC CCA GAC	239
Glu Asn Met Asp Arg Ala Ala Gln Arg Phe Arg Leu Gln Asn Pro Asp	
65 70 75	
CTG GAC TCA GAG GCG CTG CTA GCC CTG CCC CTG CCT CAG CTG GTG CAG	287

Leu	Asp	Ser	Glu	Ala	Leu	Leu	Ala	Leu	Pro	Leu	Pro	Gln	Leu	Val	Gln	
80					85				90						95	
AAG	TTA	CAC	AGT	AGA	GAG	CTG	GCC	CCT	GAG	GCC	GTG	CTC	TTC	ACC	TAT	335
Lys	Leu	His	Ser	Arg	Glu	Leu	Ala	Pro	Glu	Ala	Val	Leu	Phe	Thr	Tyr	
			100					105					110			
GTG	GGA	AAG	GCC	TGG	GAA	GTG	AAC	AAA	GGG	ACC	AAC	TGT	GTG	ACC	TCC	383
Val	Gly	Lys	Ala	Trp	Glu	Val	Asn	Lys	Gly	Thr	Asn	Cys	Val	Thr	Ser	
			115					120				125				
TAT	CTG	GCT	GAC	TGT	GAG	ACT	CAG	CTG	TCT	CAG	GCC	CCA	AGG	CAG	GGC	431
Tyr	Leu	Ala	Asp	Cys	Glu	Thr	Gln	Leu	Ser	Gln	Ala	Pro	Arg	Gln	Gly	
		130					135					140				
CTG	CTC	TAT	GGC	GTC	CCT	GTG	AGC	CTC	AAG	GAG	TGC	TTC	ACC	TAC	AAG	479
Leu	Leu	Tyr	Gly	Val	Pro	Val	Ser	Leu	Lys	Glu	Cys	Phe	Thr	Tyr	Lys	
	145					150				155						
GGC	CAG	GAC	TCC	ACG	CTG	GGC	TTG	AGC	CTG	AAT	GAA	GGG	GTG	CCG	GCG	527
Gly	Gln	Asp	Ser	Thr	Leu	Gly	Leu	Ser	Leu	Asn	Glu	Gly	Val	Pro	Ala	
160					165				170					175		
GAG	TGC	GAC	AGC	GTA	GTG	GTG	CAT	GTG	CTG	AAG	CTG	CAG	GGT	GCC	GTG	575
Glu	Cys	Asp	Ser	Val	Val	Val	His	Val	Leu	Lys	Leu	Gln	Gly	Ala	Val	
			180					185				190				
CCC	TTC	GTG	CAC	ACC	AAT	GTT	CCA	CAG	TCC	ATG	TTC	AGC	TAT	GAC	TGC	623
Pro	Phe	Val	His	Thr	Asn	Val	Pro	Gln	Ser	Met	Phe	Ser	Tyr	Asp	Cys	
			195				200					205				
AGT	AAC	CCC	CTC	TTT	GGC	CAG	ACC	GTG	AAC	CCA	TGG	AAG	TCC	TCC	AAA	671
Ser	Asn	Pro	Leu	Phe	Gly	Gln	Thr	Val	Asn	Pro	Trp	Lys	Ser	Ser	Lys	
		210					215				220					
AGC	CCA	GGG	GGC	TCC	TCA	GGG	GGT	GAA	GGG	GCC	CTC	ATC	GGG	TCT	GGA	719
Ser	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Glu	Gly	Ala	Leu	Ile	Gly	Ser	Gly	
	225					230				235						
GGC	TCC	CCC	CTG	GGC	TTA	GGC	ACT	GAT	ATC	GGA	GGC	AGC	ATC	CGC	TTC	767
Gly	Ser	Pro	Leu	Gly	Leu	Gly	Thr	Asp	Ile	Gly	Gly	Ser	Ile	Arg	Phe	
240					245				250					255		
CCC	TCC	TCC	TTC	TGC	GGC	ATC	TGC	GGC	CTC	AAG	CCC	ACA	GGG	AAC	CGC	815
Pro	Ser	Ser	Phe	Cys	Gly	Ile	Cys	Gly	Leu	Lys	Pro	Thr	Gly	Asn	Arg	
			260					265				270				
CTC	AGC	AAG	AGT	GGC	CTG	AAG	GGC	TGT	GTC	TAT	GGA	CAG	GAG	GCA	GTG	863
Leu	Ser	Lys	Ser	Gly	Leu	Lys	Gly	Cys	Val	Tyr	Gly	Gln	Glu	Ala	Val	
		275					280					285				

CGT	CTC	TCC	GTG	GGC	CCC	ATG	GCC	CGG	GAC	GTG	GAG	AGC	CTG	GCA	CTG	911
Arg	Leu	Ser	Val	Gly	Pro	Met	Ala	Arg	Asp	Val	Glu	Ser	Leu	Ala	Leu	
		290					295					300				
TGC	CTG	CGA	GCC	CTG	CTG	TGC	GAG	GAC	ATG	TTC	CGC	TTG	GAC	CCC	ACT	959
Cys	Leu	Arg	Ala	Leu	Leu	Cys	Glu	Asp	Met	Phe	Arg	Leu	Asp	Pro	Thr	
	305					310					315					
GTG	CCT	CCC	TTG	CCC	TTC	AGA	GAA	GAG	GTC	TAC	ACC	AGC	TCT	CAG	CCC	1007
Val	Pro	Pro	Leu	Pro	Phe	Arg	Glu	Glu	Val	Tyr	Thr	Ser	Ser	Gln	Pro	
320					325					330					335	
CTG	CGT	GTG	GGG	TAC	TAT	GAG	ACT	GAC	AAC	TAT	ACC	ATG	CCC	TCC	CCG	1055
Leu	Arg	Val	Gly	Tyr	Tyr	Glu	Thr	Asp	Asn	Tyr	Thr	Met	Pro	Ser	Pro	
			340					345						350		
GCC	ATG	AGG	CGG	GCC	GTG	CTG	GAG	ACC	AAA	CAG	AGC	CTT	GAG	GCT	GCG	1103
Ala	Met	Arg	Arg	Ala	Val	Leu	Glu	Thr	Lys	Gln	Ser	Leu	Glu	Ala	Ala	
			355					360						365		
GGG	CAC	ACG	CTG	GTT	CCC	TTC	TTG	CCA	AGC	AAC	ATA	CCC	CAT	GCT	CTG	1151
Gly	His	Thr	Leu	Val	Pro	Phe	Leu	Pro	Ser	Asn	Ile	Pro	His	Ala	Leu	
		370					375					380				
GAG	ACC	CTG	TCA	ACA	GGT	GGG	CTC	TTC	AGT	GAT	GGT	GGC	CAC	ACC	TTC	1199
Glu	Thr	Leu	Ser	Thr	Gly	Gly	Leu	Phe	Ser	Asp	Gly	Gly	His	Thr	Phe	
	385					390					395					
CTA	CAG	AAC	TTC	AAA	GGT	GAT	TTC	GTG	GAC	CCC	TGC	CTG	GGG	GAC	CTG	1247
Leu	Gln	Asn	Phe	Lys	Gly	Asp	Phe	Val	Asp	Pro	Cys	Leu	Gly	Asp	Leu	
400					405					410					415	
GTC	TCA	ATT	CTG	AAG	CTT	CCC	CAA	TGG	CTT	AAA	GGA	CTG	CTG	GCC	TTC	1295
Val	Ser	Ile	Leu	Lys	Leu	Pro	Gln	Trp	Leu	Lys	Gly	Leu	Leu	Ala	Phe	
			420					425						430		
CTG	GTG	AAG	CCT	CTG	CTG	CCA	AGG	CTG	TCA	GCT	TTC	CTC	AGC	AAC	ATG	1343
Leu	Val	Lys	Pro	Leu	Leu	Pro	Arg	Leu	Ser	Ala	Phe	Leu	Ser	Asn	Met	
			435					440						445		
AAG	TCT	CGT	TCG	GCT	GGA	AAA	CTC	TGG	GAA	CTG	CAG	CAC	GAG	ATC	GAG	1391
Lys	Ser	Arg	Ser	Ala	Gly	Lys	Leu	Trp	Glu	Leu	Gln	His	Glu	Ile	Glu	
		450					455					460				
GTG	TAC	CGC	AAA	ACC	GTG	ATT	GCC	CAG	TGG	AGG	GCG	CTG	GAC	CTG	GAT	1439
Val	Tyr	Arg	Lys	Thr	Val	Ile	Ala	Gln	Trp	Arg	Ala	Leu	Asp	Leu	Asp	
	465					470					475					
GTG	GTG	CTG	ACC	CCC	ATG	CTG	GCC	CCT	GCT	CTG	GAC	TTG	AAT	GCC	CCA	1487
Val	Val	Leu	Thr	Pro	Met	Leu	Ala	Pro	Ala	Leu	Asp	Leu	Asn	Ala	Pro	
480					485					490					495	

GGC AGG GCC ACA GGG GCC GTC AGC TAC ACT ATG CTG TAC AAC TGC CTG	1535
Gly Arg Ala Thr Gly Ala Val Ser Tyr Thr Met Leu Tyr Asn Cys Leu	
500 505 510	
GAC TTC CCT GCA GGG GTG GTG CCT GTC ACC ACG GTG ACT GCT GAG GAC	1583
Asp Phe Pro Ala Gly Val Val Pro Val Thr Thr Val Thr Ala Glu Asp	
515 520 525	
GAG GCC CAG ATG GAA CAT TAC AGG GGC TAC TTT GGG GAT ATC TGG GAC	1631
Glu Ala Gln Met Glu His Tyr Arg Gly Tyr Phe Gly Asp Ile Trp Asp	
530 535 540	
AAG ATG CTG CAG AAG GGC ATG AAG AAG AGT GTG GGG CTG CCG GTG GCC	1679
Lys Met Leu Gln Lys Gly Met Lys Lys Ser Val Gly Leu Pro Val Ala	
545 550 555	
GTG CAG TGT GTG GCT CTG CCC TGG CAA GAA GAG TTG TGT CTG CGG TTC	1727
Val Gln Cys Val Ala Leu Pro Trp Gln Glu Glu Leu Cys Leu Arg Phe	
560 565 570 575	
ATG CGG GAG GTG GAG CGA CTG ATG ACC CCT GAA AAG CAG TCA TCC TGATGGCTCT	1782
Met Arg Glu Val Glu Arg Leu Met Thr Pro Glu Lys Gln Ser Ser	
580 585 590	
GGCTCCAGAG GACCTGAGAC TCACACTCTC TGCAGCCCAG CCTAGTCAGG GCACAGCTGC	1842
CCTGCTGCCA CAGCAAGGAA ATGTCCTGCA TGGGGCAGAG GCTTCCGTGT CCTCTCCCCC	1902
AACCCCTGC AAGAAGCGCC GACTCCCTGA GTCTGGACCT CCATCCCTGC TCTGGTCCCC	1962
TCTCTTCGTC CTGATCCCTC CACCCCCATG TGGCAGCCCA TGGGTATGAC ATAGGCCAAG	2022
GCCCAACTAA CAGCCCCGGA ATT	2045

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Pro Gly Gly Arg Gln Gln Gln Ala Glu Gly Ile Met Val Gln Tyr Glu
1 5 10 15
Leu Trp Ala Ala Leu Pro Gly Ala Ser Gly Val Ala Leu Ala Cys Cys
20 25 30

Phe	Val	Ala	Ala	Ala	Val	Ala	Leu	Arg	Trp	Ser	Gly	Arg	Arg	Thr	Ala	35	40	45	
Arg	Gly	Ala	Val	Val	Arg	Ala	Arg	Gln	Lys	Gln	Arg	Ala	Gly	Leu	Glu	50	55	60	
Asn	Met	Asp	Arg	Ala	Ala	Gln	Arg	Phe	Arg	Leu	Gln	Asn	Pro	Asp	Leu	65	70	75	80
Asp	Ser	Glu	Ala	Leu	Leu	Ala	Leu	Pro	Leu	Pro	Gln	Leu	Val	Gln	Lys	85	90	95	
Leu	His	Ser	Arg	Glu	Leu	Ala	Pro	Glu	Ala	Val	Leu	Phe	Thr	Tyr	Val	100	105	110	
Gly	Lys	Ala	Trp	Glu	Val	Asn	Lys	Gly	Thr	Asn	Cys	Val	Thr	Ser	Tyr	115	120	125	
Leu	Ala	Asp	Cys	Glu	Thr	Gln	Leu	Ser	Gln	Ala	Pro	Arg	Gln	Gly	Leu	130	135	140	
Leu	Tyr	Gly	Val	Pro	Val	Ser	Leu	Lys	Glu	Cys	Phe	Thr	Tyr	Lys	Gly	145	150	155	160
Gln	Asp	Ser	Thr	Leu	Gly	Leu	Ser	Leu	Asn	Glu	Gly	Val	Pro	Ala	Glu	165	170	175	
Cys	Asp	Ser	Val	Val	Val	His	Val	Leu	Lys	Leu	Gln	Gly	Ala	Val	Pro	180	185	190	
Phe	Val	His	Thr	Asn	Val	Pro	Gln	Ser	Met	Phe	Ser	Tyr	Asp	Cys	Ser	195	200	205	
Asn	Pro	Leu	Phe	Gly	Gln	Thr	Val	Asn	Pro	Trp	Lys	Ser	Ser	Lys	Ser	210	215	220	
Pro	Gly	Gly	Ser	Ser	Gly	Gly	Glu	Gly	Ala	Leu	Ile	Gly	Ser	Gly	Gly	225	230	235	240
Ser	Pro	Leu	Gly	Leu	Gly	Thr	Asp	Ile	Gly	Gly	Ser	Ile	Arg	Phe	Pro	245	250	255	
Ser	Ser	Phe	Cys	Gly	Ile	Cys	Gly	Leu	Lys	Pro	Thr	Gly	Asn	Arg	Leu	260	265	270	
Ser	Lys	Ser	Gly	Leu	Lys	Gly	Cys	Val	Tyr	Gly	Gln	Glu	Ala	Val	Arg	275	280	285	
Leu	Ser	Val	Gly	Pro	Met	Ala	Arg	Asp	Val	Glu	Ser	Leu	Ala	Leu	Cys	290	295	300	

Leu	Arg	Ala	Leu	Leu	Cys	Glu	Asp	Met	Phe	Arg	Leu	Asp	Pro	Thr	Val	
305					310					315					320	
Pro	Pro	Leu	Pro	Phe	Arg	Glu	Glu	Val	Tyr	Thr	Ser	Ser	Gln	Pro	Leu	
				325					330					335		
Arg	Val	Gly	Tyr	Tyr	Glu	Thr	Asp	Asn	Tyr	Thr	Met	Pro	Ser	Pro	Ala	
			340					345					350			
Met	Arg	Arg	Ala	Val	Leu	Glu	Thr	Lys	Gln	Ser	Leu	Glu	Ala	Ala	Gly	
		355					360					365				
His	Thr	Leu	Val	Pro	Phe	Leu	Pro	Ser	Asn	Ile	Pro	His	Ala	Leu	Glu	
	370					375					380					
Thr	Leu	Ser	Thr	Gly	Gly	Leu	Phe	Ser	Asp	Gly	Gly	His	Thr	Phe	Leu	
385				390						395					400	
Gln	Asn	Phe	Lys	Gly	Asp	Phe	Val	Asp	Pro	Cys	Leu	Gly	Asp	Leu	Val	
			405						410					415		
Ser	Ile	Leu	Lys	Leu	Pro	Gln	Trp	Leu	Lys	Gly	Leu	Leu	Ala	Phe	Leu	
		420						425					430			
Val	Lys	Pro	Leu	Leu	Pro	Arg	Leu	Ser	Ala	Phe	Leu	Ser	Asn	Met	Lys	
		435					440					445				
Ser	Arg	Ser	Ala	Gly	Lys	Leu	Trp	Glu	Leu	Gln	His	Glu	Ile	Glu	Val	
	450					455					460					
Tyr	Arg	Lys	Thr	Val	Ile	Ala	Gln	Trp	Arg	Ala	Leu	Asp	Leu	Asp	Val	
465				470						475					480	
Val	Leu	Thr	Pro	Met	Leu	Ala	Pro	Ala	Leu	Asp	Leu	Asn	Ala	Pro	Gly	
			485						490					495		
Arg	Ala	Thr	Gly	Ala	Val	Ser	Tyr	Thr	Met	Leu	Tyr	Asn	Cys	Leu	Asp	
		500						505					510			
Phe	Pro	Ala	Gly	Val	Val	Pro	Val	Thr	Thr	Val	Thr	Ala	Glu	Asp	Glu	
		515					520					525				
Ala	Gln	Met	Glu	His	Tyr	Arg	Gly	Tyr	Phe	Gly	Asp	Ile	Trp	Asp	Lys	
	530					535					540					
Met	Leu	Gln	Lys	Gly	Met	Lys	Lys	Ser	Val	Gly	Leu	Pro	Val	Ala	Val	
545					550					555					560	
Gln	Cys	Val	Ala	Leu	Pro	Trp	Gln	Glu	Glu	Leu	Cys	Leu	Arg	Phe	Met	
			565					570						575		

Arg Glu Val Glu Arg Leu Met Thr Pro Glu Lys Gln Ser Ser
580 585 590

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2045 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATTCCGGGG CTGTTAGTTG GGCCTTGGCC TATGTCATAC CCATGGGCTG CCACATGGGG	60
GTGGAGGGGAT CAGGACGAAG AGAGGGGACC AGAGCAGGGA TGGAGGTCCA GACTCAGGGA	120
GTCGGCGCTT CTTGCAGGGG GTTGGGGGAG AGGACACGGA AGCCTCTGCC CCATGCAGGA	180
CATTTCTTTG CTGTGGCAGC AGGGCAGCTG TGCCCTGACT AGGCTGGGCT GCAGAGAGTG	240
TGAGTCTCAG GTCCTCTGGA GCCAGAGCCA TCAGGATGAC TGCTTTTCAG GGGTCATCAG	300
TCGCTCCACC TCCCGCATGA ACCGCAGACA CAACTCTTCT TGCCAGGGCA GAGCCACACA	360
CTGCACGGCC ACCGGCAGCC CCACACTCTT CTTTCATGCCC TTCTGCAGCA TCTTGTCCCA	420
GATATCCCCA AAGTAGCCCC TGTAATGTTT CATCTGGGCC TCGTCCTCAG CAGTCACCGT	480
GGTGACAGGC ACCACCCCTG CAGGGAAGTC CAGGCAGTTG TACAGCATAG TGTAGCTGAC	540
GGCCCCGTGT GCCCTGCCTG GGGCATTCAA GTCCAGAGCA GGGGCCAGCA TGGGGGTCAG	600
CACCACATCC AGGTCCAGCG CCCTCCACTG GGCAATCACG GTTTTGCGGT ACACCTCGAT	660
CTCGTGCTGC AGTTCCCAGA GTTTTCCAGC CGAACGAGAC TTCATGTTGC TGAGGAAAGC	720
TGACAGCCTT GGCAGCAGAG GCTTCACCAG GAAGGCCAGC AGTCCTTTAA GCCATTGGGG	780
AAGCTTCAGA ATTGAGACCA GTTCCCCAG GCAGGGGTCC ACGAAATCAC CTTTGAAGTT	840
CTGTAGGAAG GTGTGGCCAC CATCACTGAA GAGCCACCT GTTGACAGGG TCTCCAGAGC	900

ATGGGGTATG TTGCTTGGCA AGAAGGGAAC CAGCGTGTGC CCCGCAGCCT CAAGGCTCTG	960
TTTGGTCTCC AGCACGGCCC GCCTCATGGC CGGGGAGGGC ATGGTATAGT TGTCAGTCTC	1020
ATAGTACCCC ACACGCAGGG GCTGAGAGCT GGTGTAGACC TCTTCTCTGA AGGGCAAGGG	1080
AGGCACAGTG GGGTCCAAGC GGAACATGTC CTCGCACAGC AGGGCTCGCA GGCACAGTGC	1140
CAGGCTCTCC ACGTCCCGGG CCATGGGGCC CACGGAGAGA CGCACTGCCT CCTGTCCATA	1200
GACACAGCCC TTCAGGCCAC TCTTGCTGAG GCGGTTCCCT GTGGGCTTGA GGCCGCAGAT	1260
GCCGCAGAAG GAGGAGGGGA AGCGGATGCT GCCTCCGATA TCAGTGCCTA AGCCCAGGGG	1320
GGAGCCTCCA GACCCGATGA GGGCCCCCTC ACCCCCTGAG GAGCCCCCTG GGCTTTTGA	1380
GGACTTCCAT GGGTTCACGG TCTGGCCAAA GAGGGGGTTA CTGCAGTCAT AGCTGAACAT	1440
GGACTGTGGA ACATTGGTGT GCACGAAGGG CACGGCACCC TGCAGCTTCA GCACATGCAC	1500
CACTACGCTG TCGCACTCCG CCGGCACCCC TTCATTGAG CTCAAGCCCA GCGTGGAGTC	1560
CTGGCCCTTG TAGGTGAAGC ACTCCTTGAG GCTCACAGGG ACGCCATAGA GCAGGCCCTG	1620
CCTTGGGGCC TGAGACAGCT GAGTCTCACA GTCAGCCAGA TAGGAGGTCA CACAGTTGGT	1680
CCCTTTGTTC ACTTCCCAGG CCTTTCCCAC ATAGGTGAAG AGCACGGCCT CAGGGGCCAG	1740
CTCTCTACTG TGTAACCTTCT GCACCAGCTG AGGCAGGGGC AGGGCTAGCA GCGCCTCTGA	1800
GTCCAGGTCT GGGTTCTGGA GCCGGAAGCG CTGCGCCGCC CTGTCCATGT TCTCCAGGCC	1860
CGCTCGCTGC TTCTGTCGCG CCCGGACCAC CGCGCCCCGC GCCGTCCGGC GCCCGGACCA	1920
GCGCAGGGCC ACGGCCGCCG CCACGAAGCA GCAGGCCAGG GCGACCCCGG AGGCGCCAGG	1980
CAGCGCGGCC CACAGCTCGT ACTGCACCAT GATCCCTTCA GCCTGCTGCT GCCTACCGCC	2040
CGGCA	2045

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCGGTACCAT GCGATGGACC GGGCGC

26

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTGGCCA AAGAGAGG

18

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Ala Gly Gly Gly Ser
1 5 10 15

Leu Leu Gly Ile Gly Ser Asp Val Ala Gly Ser Ile Arg Leu Pro Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ala Gly Gly Ser
1 5 10 15

Leu Ile Gly Ile Gly Thr Asp Val Gly Gly Ser Val Arg Ile Pro Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Gly Gly Ser Ser Gly Gly Glu Ser Ala Leu Ile Ser Ala Asp Gly Ser
1 5 10 15

Leu Leu Gly Ile Gly Gly Asp Val Gly Gly Ser Ile Arg Ile Pro Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gly Ser Ser Gly Gly Glu Gly Ser Leu Ile Gly Ala His Gly Ser
1 5 10 15

Leu Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Ile Pro Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gly Gly Ser Ser Gly Gly Glu Gly Ala Ile Val Gly Ile Arg Gly Gly
1 5 10 15

Val Ile Gly Val Gly Thr Asp Ile Gly Gly Ser Ile Asp Val Pro Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Gly Ser Ser Gly Gly Val Ala Ala Ala Val Ala Ser Arg Leu Met

1	5	10	15
Leu Gly Gly Ile Gly Thr Asp Thr Gly Ala Ser Val Arg Leu Pro Ala			
20	25	30	

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Gly Gly Ser Ser Gly Gly Val Ala Ala Ala Val Ala Ser Gly Ile Val			
1	5	10	15
Pro Leu Ser Val Gly Thr Asp Thr Gly Gly Ser Ile Arg Ile Pro Ala			
20	25	30	

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCAGGAGGTT CCTCAGGGGG TGAGGGGGCT CTCATTGGAT CTGGAGGTTT CCCTCTGGGT	60
TTAGGCACTG ACATTGGCGG CAGCATCCGG TTCCCTTCTG CTTTCTGCGG CATCTGTGGC	120
CTCAAGCCTA CTGGCAACCG CCTCAGCAAG AGTGGCCTGA AGGGCTGTGT CTATGGACAG	180

ACGGCAGTGC AGCTTTCTCT TGGCCCCATG GCCCAGGATG TGGAGAGCCT GCGCTATGC	240
CTGAAAGCTC TACTGTGTGA GCACTTGTTT AECTTGGACC CTACCGTGCC TCCCTTTCCC	300
TTCAGAGAGG AGGTCTATAG AAGTTCTAGA CCCCTGCGTG TGGGGTACTA TGAGACTGAC	360
AACTATACCA TGCCCAGCCC AGCTATGAGG AGGGCTCTGA TAGAGACCAA GCAGAGACTT	420
GAGGCTGCTG GCCACACGCT GATTCCCTTC TTACCCAACA ACATACCCTA CGCCCTGGAG	480
GTCCTGTCTG CGGGCGGCCT GTTCAGTGAC GGTGGCCGCA GTTTTCTCCA AACTTCAAA	540
GGTGACTTTG TGGATCCCTG CTTGGGAGAC CTGATCTTAA TTCTGAGGCT GCCCAGCTGG	600
TTTAAAAGAC TGCTGAGCCT CCTGCTGAAG CCTCTGTTTC CTCGGCTGGC AGCCTTTCTC	660
AACAGTATGC GTCCTCGGTC AGCTGAAAAG CTGTGGAAAC TGCAGCATGA GATTGAGATG	720
TATCGCCAGT CTGTGATTGC CCAGTGGAAA GCGATGAACT TGGATGTGCT GCTGACCCCN	780
ATGYTNGGNC CNGCNYTNGA YYTNAAYACN -CCNGGNMGN	819